

Supplementary Information

The journey of HIV-1 non-nucleoside reverse transcriptase inhibitors (NNRTIs) from lab to clinic

Vigneshwaran Namasivayam^{1*}, Murugesan Vanangamudi², Victor G. Kramer³, Sonali Kurup^{4§}, Peng Zhan⁵, Xinyong Liu⁵, Jacob Kongsted⁶, Siddappa N. Byrareddy⁷

¹Pharmaceutical Institute, Pharmaceutical Chemistry II, University of Bonn, 53121 Bonn.
Germany.

²Department of Medicinal and Pharmaceutical Chemistry, SreeVidyanikethan College of
Pharmacy, Tirupathi, Andhra Pradesh 517102. India.

³Merck Canada Inc., Kirkland, Quebec H9H 4M7. Canada.

⁴College of Pharmacy, Roosevelt University, Schaumburg, Illinois 60173. USA.

⁵Department of Medicinal Chemistry, Key Laboratory of Chemical Biology (Ministry of
Education), School of Pharmaceutical Sciences, Shandong University, 44, West Culture Road,
Jinan 250012. PR China.

⁶Department of Physics, Chemistry and Pharmacy, University of Southern Denmark, DK-5230,
Odense M. Denmark.

⁷Department of Pharmacology and Experimental Neuroscience, University of Nebraska Medical
Center, Omaha 68198-5880. USA.

§Present address: Ferris State University, 220 Ferris Drive, Big Rapids, Michigan 49307.

Table of contents

Table S1: Published X-ray Crystal Structures of HIV-1 Reverse Transcriptase (RT) with the approved NNRTI drugs.....	S3
Figure S1: Metabolic pathway of DLV and various key metabolic sites are highlighted are in yellow and cyan colors.....	S5
Figure S2: Metabolic pathway of EFV and various key metabolic sites are highlighted are in yellow and cyan colors.....	S6
Figure S3: Metabolic pathway of ETR and various key metabolic sites are highlighted are in yellow and cyan colors.....	S7
Figure S4: Metabolic pathways of RPV and key metabolic sites are highlighted are in yellow and cyan colors.....	S8
References	S9

Table S1: Published X-ray Crystal Structures of HIV-1 Reverse Transcriptase (RT) with the approved NNRTI drugs

PDB ID	NNRTI	Resolution (Å)	HIV-1 RT	Release Year	Reference
3HVT	NVP	2.90	wild-type	1994	¹
1VRT	NVP	2.20	wild-type	1996	²
1FKP	NVP	2.90	K103N	2000	³
1JLB	NVP	3.00	Y181C	2001	⁴
1JLF	NVP	2.60	Y188C	2001	⁴
1LW0	NVP	2.80	T215Y	2002	⁵
1LWC	NVP	2.62	M184V	2002	⁵
1LWE	NVP	2.81	M41L/T215Y RTMQ+M184V	2002	⁵
1LWF	NVP	2.80	M41L/D67N/K70R/ M184V/T215Y	2002	⁵
1S1U	NVP	3.00	L100I	2004	⁶
1S1X	NVP	2.80	V108I	2004	⁶
2HND	NVP	2.50	K101E	2006	⁷
2HNY	NVP	2.50	E138K	2006	⁷
3LP0	NVP	2.79	wild-type	2010	⁸
3LP1	NVP	2.23	wild-type	2010	⁸
3QIP	NVP	2.09	wild-type	2011	⁹
3V81	NVP	2.85	wild-type	2012	¹⁰
4B3Q	NVP	5.00	wild-type	2013	¹¹
4PUO	NVP	2.90	wild-type	2014	¹²
4PWD	NVP	3.00	wild-type	2014	¹²
4Q0B	NVP	3.30	wild-type	2014	¹²
5HBM	NVP	3.04	wild-type	2016	unpublished
1KLM	DLV	2.65	wild-type	1998	¹³
1FK9	EFV	2.50	wild-type	2000	³
1FKO	EFV	2.90	K103N	2000	³
1IKV	EFV	3.00	K103N	2001	⁴
1IKW	EFV	3.00	wild-type	2001	⁴
1JKH	EFV	2.50	Y181C	2001	⁴
4B3O	EFV	3.30	wild-type	2013	¹¹
6BSG	EFV	2.44	wild-type	2018	unpublished
6BSH	EFV	2.65	wild-type	2018	unpublished
6BSI	EFV	3.25	wild-type	2018	unpublished
6BSJ	EFV	2.89	wild-type	2018	unpublished
1SV5	ETV	2.90	K103N	2004	¹⁴
3M8P	ETV	2.67	wild-type	2010	¹⁵
3MEC	ETV	2.30	wild-type	2010	¹⁶

3MED	ETV	2.50	K103N	2010	¹⁶
2ZD1	RPV	1.80	wild-type	2008	¹⁷
2ZE2	RPV	2.90	L100I/K103N	2008	¹⁷
3BGR	RPV	2.10	K103N/Y181C	2008	¹⁷
3MEE	RPV	2.40	wild-type	2010	¹⁸
3MEG	RPV	2.80	K103N	2010	¹⁸
3QLH	RPV	2.70	wild-type	2011	¹⁹
4G1Q	RPV	1.51	wild-type	2013	²⁰
4ICL	RPV	1.80	wild-type	2013	²⁰
4ID5	RPV	1.95	wild-type	2013	²⁰
4IDK	RPV	2.10	wild-type	2013	²⁰
4IFV	RPV	2.05	wild-type	2013	²⁰
4IFY	RPV	2.10	wild-type	2013	²⁰
4IG3	RPV	1.95	wild-type	2013	²⁰
4KFB	RPV	1.85	wild-type	2013	²⁰

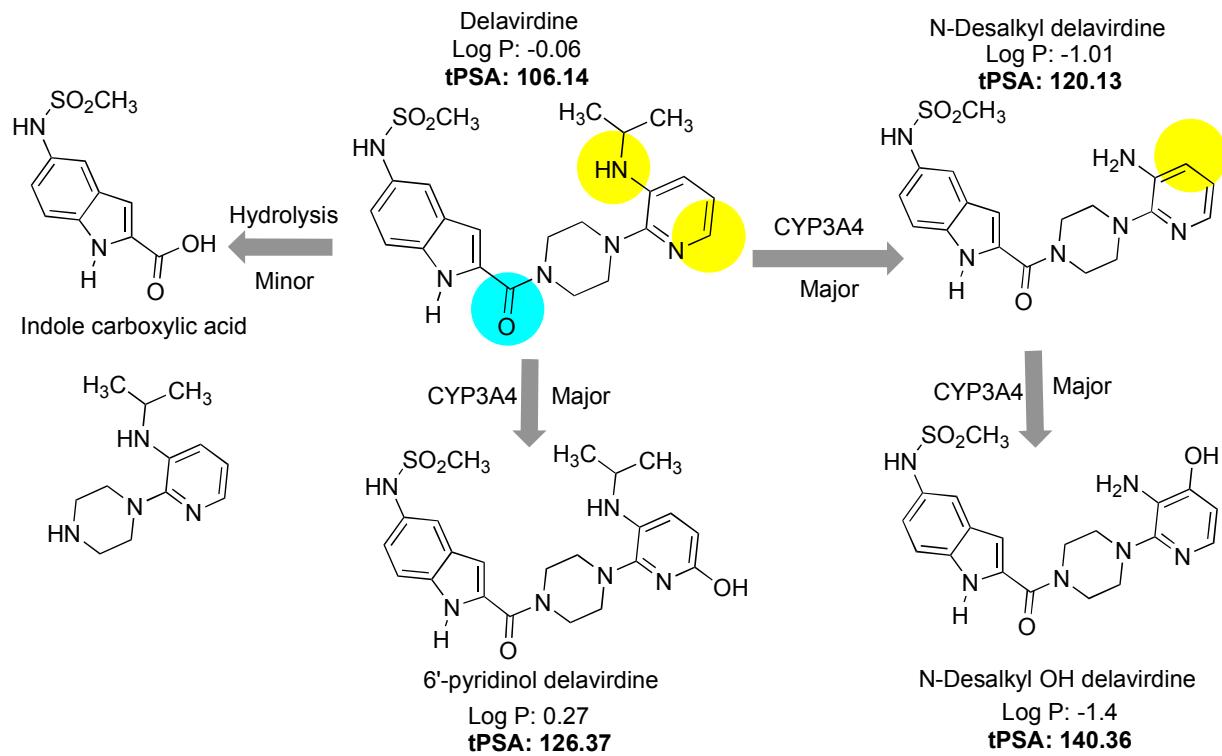


Figure S1: Metabolic pathway of DLV and various key metabolic sites are highlighted are in yellow and cyan colors.

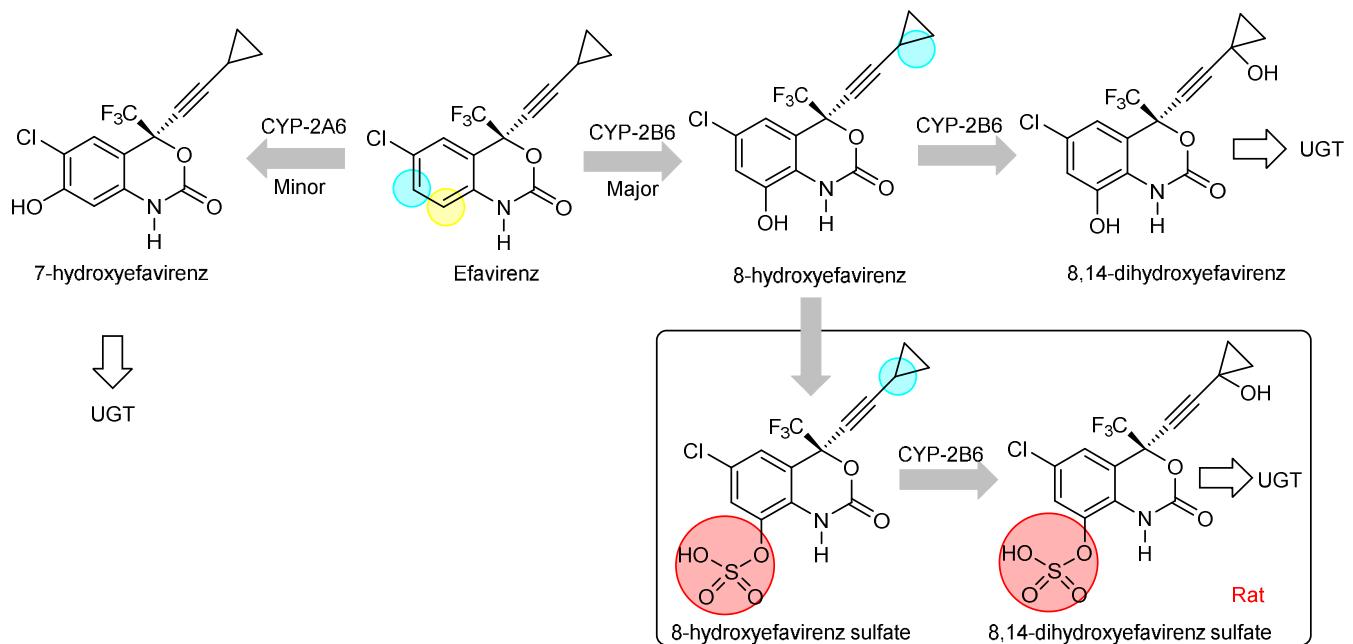


Figure S2: Metabolic pathway of EFV and various key metabolic sites are highlighted are in yellow and cyan colors.

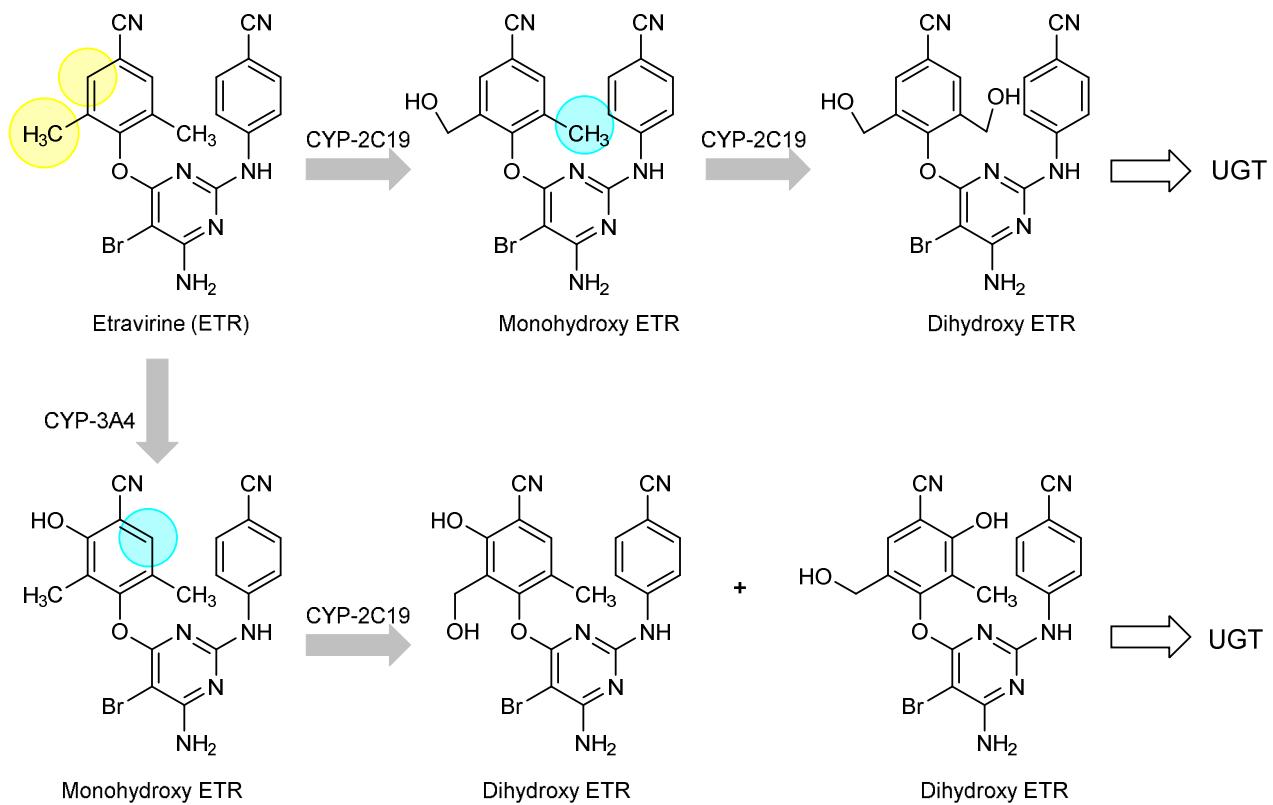


Figure S3: Metabolic pathway of ETR and various key metabolic sites are highlighted are in yellow and cyan colors

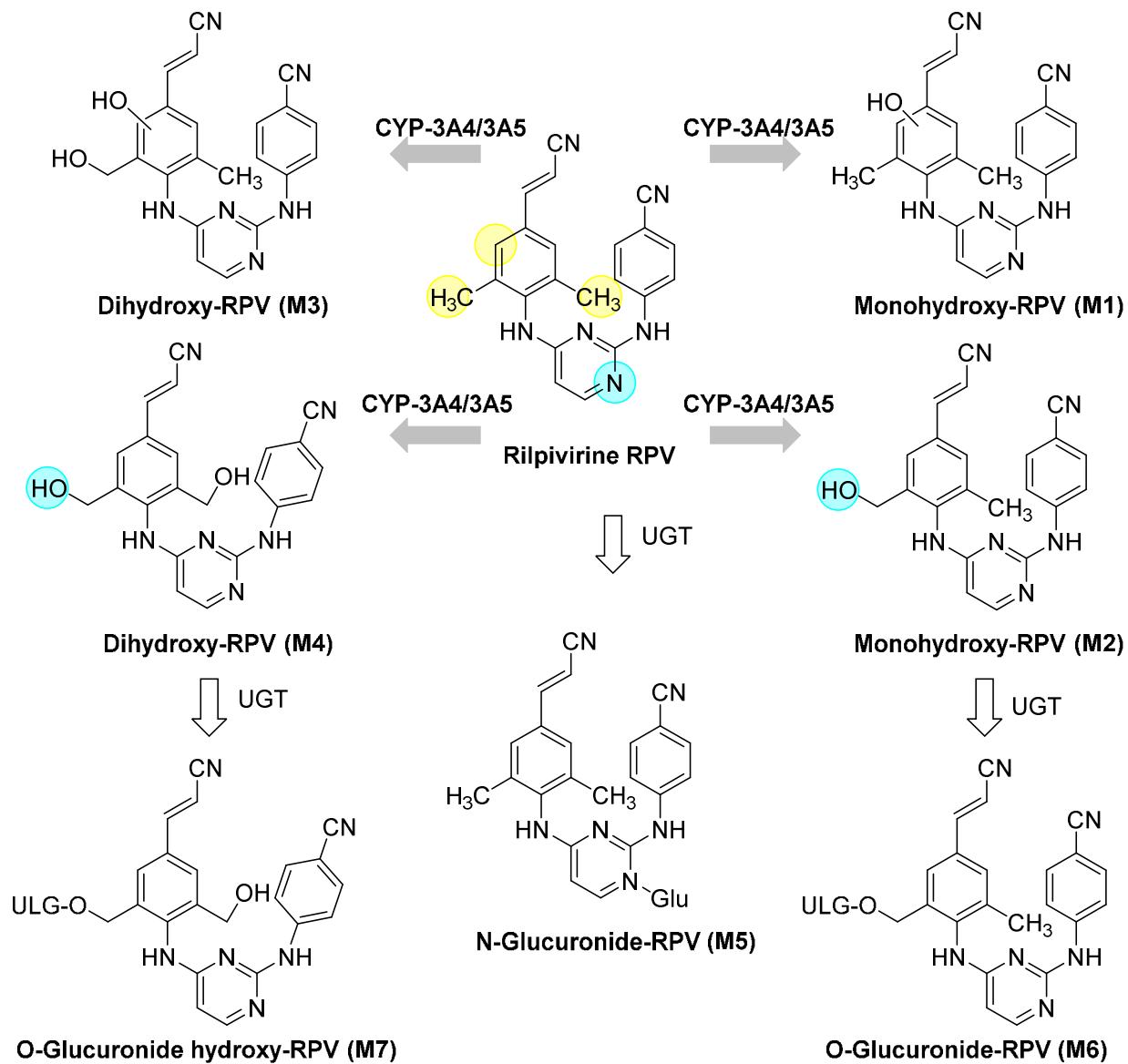


Figure S4: Metabolic pathways of RPV and key metabolic sites are highlighted are in yellow and cyan colors

References:

1. Smerdon, S. J.; Jager, J.; Wang, J.; Kohlstaedt, L. A.; Chirino, A. J.; Friedman, J. M.; Rice, P. A.; Steitz, T. A., Structure of the binding site for nonnucleoside inhibitors of the reverse transcriptase of human immunodeficiency virus type 1. *Proc. Natl. Acad. Sci. U. S. A.* **1994**, *91* (9), 3911-3915.
2. Ren, J.; Esnouf, R.; Garman, E.; Somers, D.; Ross, C.; Kirby, I.; Keeling, J.; Darby, G.; Jones, Y.; Stuart, D.; et al., High resolution structures of HIV-1 RT from four RT-inhibitor complexes. *Nat. Struct. Biol.* **1995**, *2* (4), 293-302.
3. Ren, J.; Milton, J.; Weaver, K. L.; Short, S. A.; Stuart, D. I.; Stammers, D. K., Structural basis for the resilience of efavirenz (DMP-266) to drug resistance mutations in HIV-1 reverse transcriptase. *Structure* **2000**, *8* (10), 1089-1094.
4. Ren, J.; Nichols, C.; Bird, L.; Chamberlain, P.; Weaver, K.; Short, S.; Stuart, D. I.; Stammers, D. K., Structural mechanisms of drug resistance for mutations at codons 181 and 188 in HIV-1 reverse transcriptase and the improved resilience of second generation non-nucleoside inhibitors. *J. Mol. Biol.* **2001**, *312* (4), 795-805.
5. Chamberlain, P. P.; Ren, J.; Nichols, C. E.; Douglas, L.; Lennerstrand, J.; Larder, B. A.; Stuart, D. I.; Stammers, D. K., Crystal structures of Zidovudine- or Lamivudine-resistant human immunodeficiency virus type 1 reverse transcriptases containing mutations at codons 41, 184, and 215. *J. Virol.* **2002**, *76* (19), 10015-10019.
6. Ren, J.; Nichols, C. E.; Chamberlain, P. P.; Weaver, K. L.; Short, S. A.; Stammers, D. K., Crystal structures of HIV-1 reverse transcriptases mutated at codons 100, 106 and 108 and mechanisms of resistance to non-nucleoside inhibitors. *J. Mol. Biol.* **2004**, *336* (3), 569-578.

7. Ren, J.; Nichols, C. E.; Stamp, A.; Chamberlain, P. P.; Ferris, R.; Weaver, K. L.; Short, S. A.; Stammers, D. K., Structural insights into mechanisms of non-nucleoside drug resistance for HIV-1 reverse transcriptases mutated at codons 101 or 138. *Febs J.* **2006**, *273* (16), 3850-3860.
8. Su, H. P.; Yan, Y.; Prasad, G. S.; Smith, R. F.; Daniels, C. L.; Abeywickrema, P. D.; Reid, J. C.; Loughran, H. M.; Kornienko, M.; Sharma, S.; Grobler, J. A.; Xu, B.; Sardana, V.; Allison, T. J.; Williams, P. D.; Darke, P. L.; Hazuda, D. J.; Munshi, S., Structural basis for the inhibition of RNase H activity of HIV-1 reverse transcriptase by RNase H active site-directed inhibitors. *J. Virol.* **2010**, *84* (15), 7625-7633.
9. Lansdon, E. B.; Liu, Q.; Leavitt, S. A.; Balakrishnan, M.; Perry, J. K.; Lancaster-Moyer, C.; Kutty, N.; Liu, X.; Squires, N. H.; Watkins, W. J.; Kirschberg, T. A., Structural and binding analysis of pyrimidinol carboxylic acid and N-hydroxy quinazolinedione HIV-1 RNase H inhibitors. *Antimicrob. Agents Chemother.* **2011**, *55* (6), 2905-2915.
10. Das, K.; Martinez, S. E.; Bauman, J. D.; Arnold, E., HIV-1 reverse transcriptase complex with DNA and nevirapine reveals non-nucleoside inhibition mechanism. *Nat. Struct. Mol. Biol.* **2012**, *19* (2), 253-259.
11. Lapkouski, M.; Tian, L.; Miller, J. T.; Le Grice, S. F. J.; Yang, W., Complexes of HIV-1 RT, NNRTI and RNA/DNA hybrid reveal a structure compatible with RNA degradation. *Nat. Struct. Mol. Biol.* **2013**, *20* (2), 230-236.
12. Das, K.; Martinez, S. E.; Bandwar, R. P.; Arnold, E., Structures of HIV-1 RT-RNA/DNA ternary complexes with dATP and nevirapine reveal conformational flexibility of RNA/DNA: insights into requirements for RNase H cleavage. *Nucleic Acids Res.* **2014**, *42* (12), 8125-8137.
13. Esnouf, R. M.; Ren, J.; Hopkins, A. L.; Ross, C. K.; Jones, E. Y.; Stammers, D. K.; Stuart, D. I., Unique features in the structure of the complex between HIV-1 reverse transcriptase

and the bis(heteroaryl)piperazine (BHAP) U-90152 explain resistance mutations for this nonnucleoside inhibitor. *Proc. Natl. Acad. Sci. U. S. A.* **1997**, *94* (8), 3984-3989.

14. Das, K.; Clark, A. D., Jr.; Lewi, P. J.; Heeres, J.; De Jonge, M. R.; Koymans, L. M.; Vinkers, H. M.; Daeyaert, F.; Ludovici, D. W.; Kukla, M. J.; De Corte, B.; Kavash, R. W.; Ho, C. Y.; Ye, H.; Lichtenstein, M. A.; Andries, K.; Pauwels, R.; De Bethune, M. P.; Boyer, P. L.; Clark, P.; Hughes, S. H.; Janssen, P. A.; Arnold, E., Roles of conformational and positional adaptability in structure-based design of TMC125-R165335 (etravirine) and related non-nucleoside reverse transcriptase inhibitors that are highly potent and effective against wild-type and drug-resistant HIV-1 variants. *J. Med. Chem.* **2004**, *47* (10), 2550-2560.
15. Kertesz, D. J.; Brotherton-Pleiss, C.; Yang, M.; Wang, Z.; Lin, X.; Qiu, Z.; Hirschfeld, D. R.; Gleason, S.; Mirzadegan, T.; Dunten, P. W.; Harris, S. F.; Villasenor, A. G.; Hang, J. Q.; Heilek, G. M.; Klumpp, K., Discovery of piperidin-4-yl-aminopyrimidines as HIV-1 reverse transcriptase inhibitors. N-benzyl derivatives with broad potency against resistant mutant viruses. *Bioorg. Med. Chem. Lett.* **2010**, *20* (14), 4215-4218.
16. Lansdon, E. B.; Brendza, K. M.; Hung, M.; Wang, R.; Mukund, S.; Jin, D.; Birkus, G.; Kutty, N.; Liu, X., Crystal structures of HIV-1 reverse transcriptase with etravirine (TMC125) and rilpivirine (TMC278): implications for drug design. *J. Med. Chem.* **2010**, *53* (10), 4295-4299.
17. Das, K.; Bauman, J. D.; Clark, A. D., Jr.; Frenkel, Y. V.; Lewi, P. J.; Shatkin, A. J.; Hughes, S. H.; Arnold, E., High-resolution structures of HIV-1 reverse transcriptase/TMC278 complexes: strategic flexibility explains potency against resistance mutations. *Proc. Natl. Acad. Sci. U. S. A.* **2008**, *105* (5), 1466-1471.
18. Lansdon, E. B.; Brendza, K. M.; Hung, M.; Wang, R.; Mukund, S.; Jin, D.; Birkus, G.; Kutty, N.; Liu, X., Crystal structures of HIV-1 reverse transcriptase with etravirine (TMC125) and rilpivirine (TMC278): implications for drug design. *J. Med. Chem.* **2010**, *53* (10), 4295-429.

19. Chung, S.; Himmel, D. M.; Jiang, J. K.; Wojtak, K.; Bauman, J. D.; Rausch, J. W.; Wilson, J. A.; Beutler, J. A.; Thomas, C. J.; Arnold, E.; Le Grice, S. F., Synthesis, activity, and structural analysis of novel alpha-hydroxytropolone inhibitors of human immunodeficiency virus reverse transcriptase-associated ribonuclease H. *J. Med. Chem.* **2011**, *54* (13), 4462-4473.
20. Bauman, J. D.; Patel, D.; Dharia, C.; Fromer, M. W.; Ahmed, S.; Frenkel, Y.; Vijayan, R. S.; Eck, J. T.; Ho, W. C.; Das, K.; Shatkin, A. J.; Arnold, E., Detecting allosteric sites of HIV-1 reverse transcriptase by X-ray crystallographic fragment screening. *J. Med. Chem.* **2013**, *56* (7), 2738-2746.